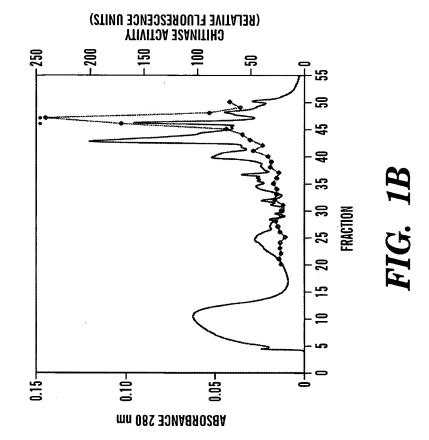
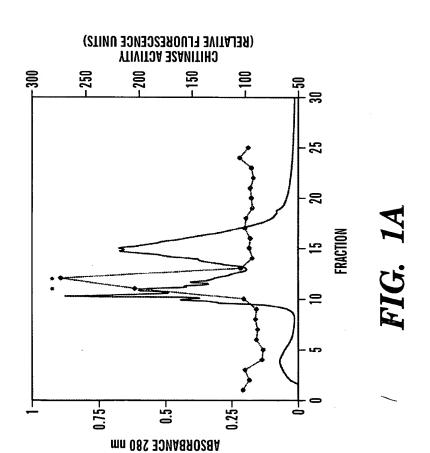


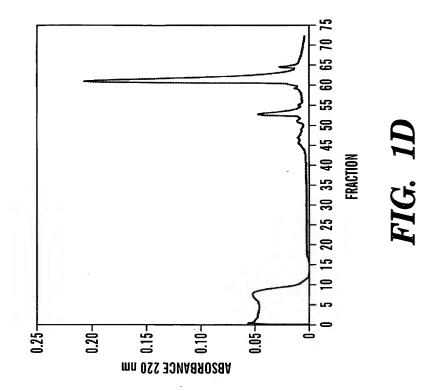
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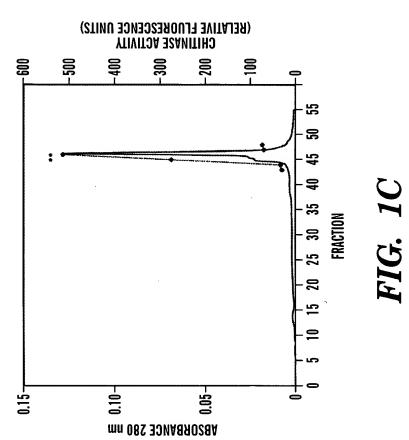






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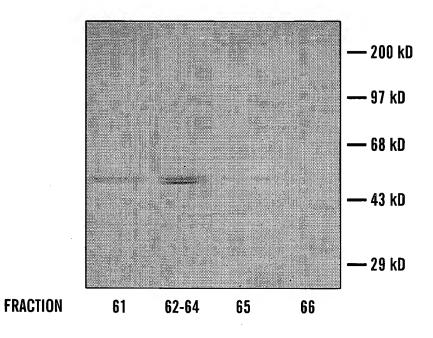


FIG. 1E

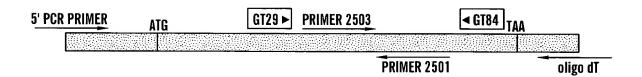


FIG. 2



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MNFKISIFLIIVSILYSANSRICKGKNNINNSLGIIRENKNKTHOTEIHE	50
N-terminal 1 N-terminal 2	
SFSHLKSNNSNFVETYGSYCGDGCNSTRITKNNKNINKNDRKSPROILEEYK	100
KRKQGIIAGYYGSWNSQGDRAKHMIDSNPMVSILYIAFARINMLYDVSRP	150
Substrate binding site FNGRQRFLLRKHGLEYETYGMMLNEIRRIRKVRPDVLILLSLGGETYMID Active site peptide	200
I EKE I DYVDK I LKL VND BUDGVO I OWEPHGKFYNLNELNFSNYY I KL I N Catalytic active site	250
LLRKTIPEEKLISISGSSNAALSCVSGVASFCKDEESPYNTKFLSEQIET	300
NKELHRAAAMLSAGTFINIFNTAKEKIDLVFIQTYNLETTNPDIMVDMYL	350
SHLYFGLKYNITIILGFSLEHNRGGFSPENKELLELVGKTIHDKNONNNR	400
ADGIGIWHLFMKEQLPTGSFDVDIFLTNIWKHLNPEVQTPKDLTITENPE GT33	450
DCSTIDEYVPGLVIPTIGIYYKHNDAIWKTRSYSIHAPGVDRYEWDLVKV	500
CYEKICDGKAAHYYNTDYKESSIIIWKGEPYLIKWWQQGPPEGQALESYT GT29	550
KLUASKCPGIEEWNKK <u>YPHKPLEVEEQY</u> EQEVDLPLQ* GT84	587

FIG. 3





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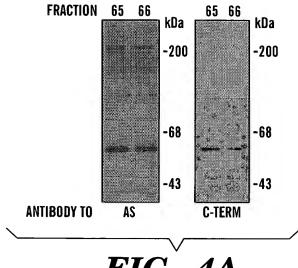


FIG. 4A

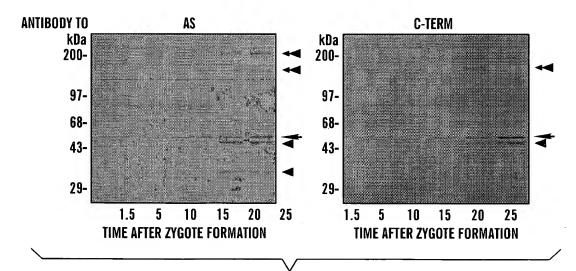


FIG. 4B

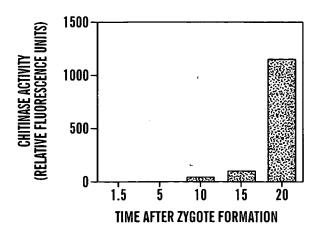
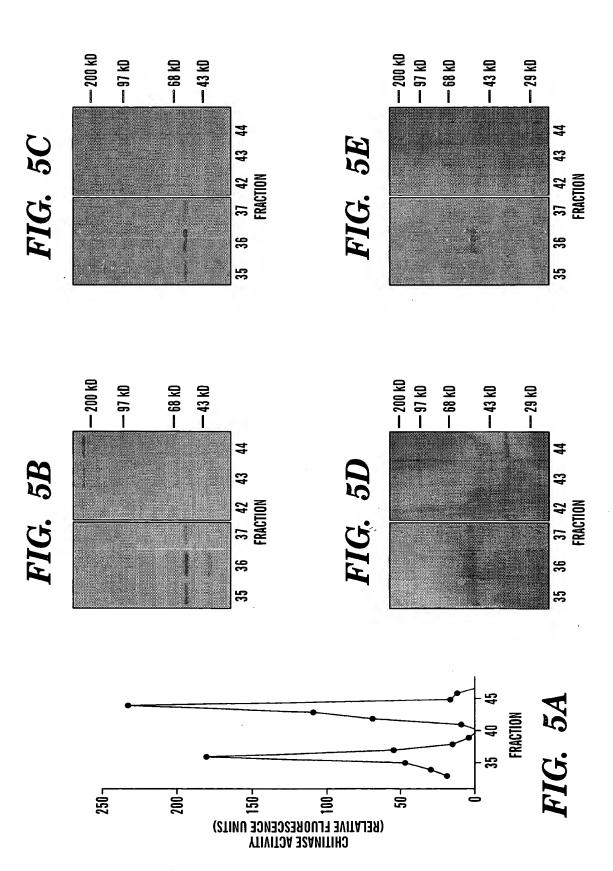
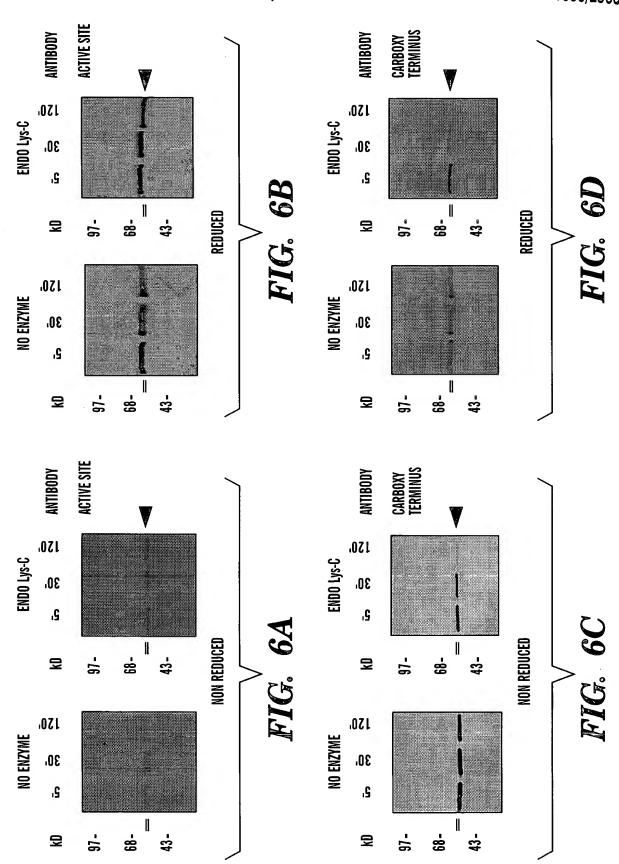


FIG. 4C

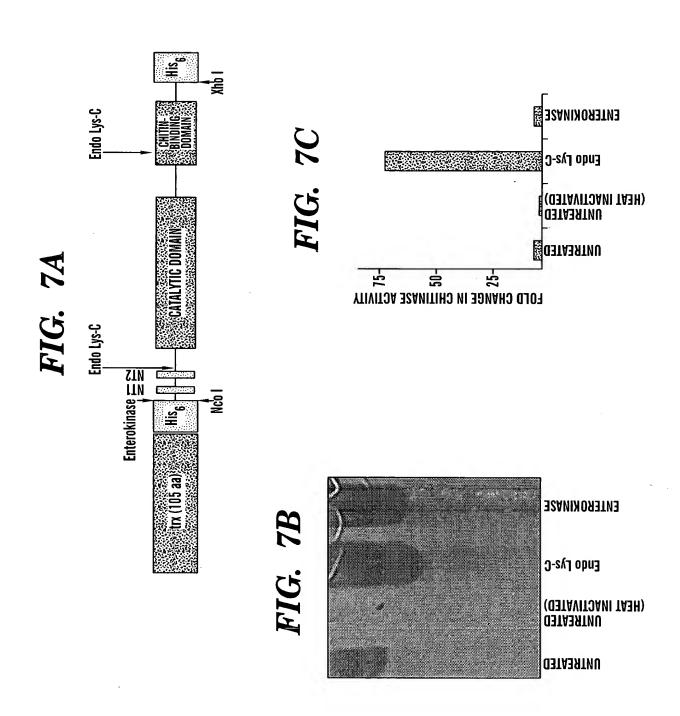


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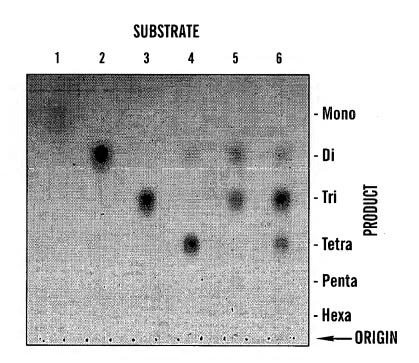
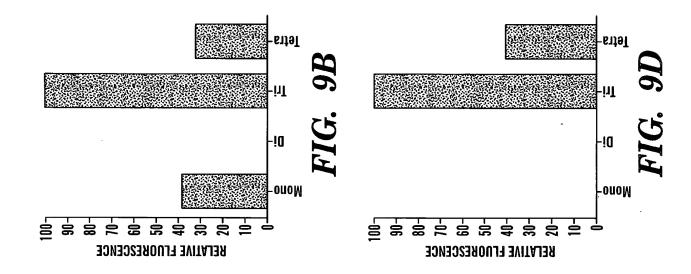


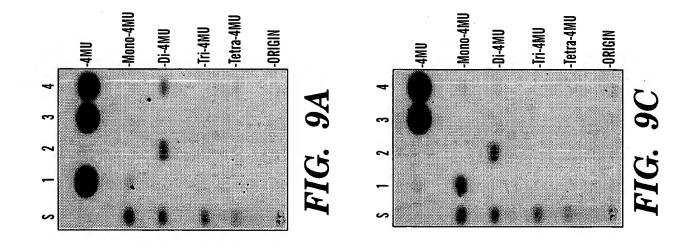
FIG. 8



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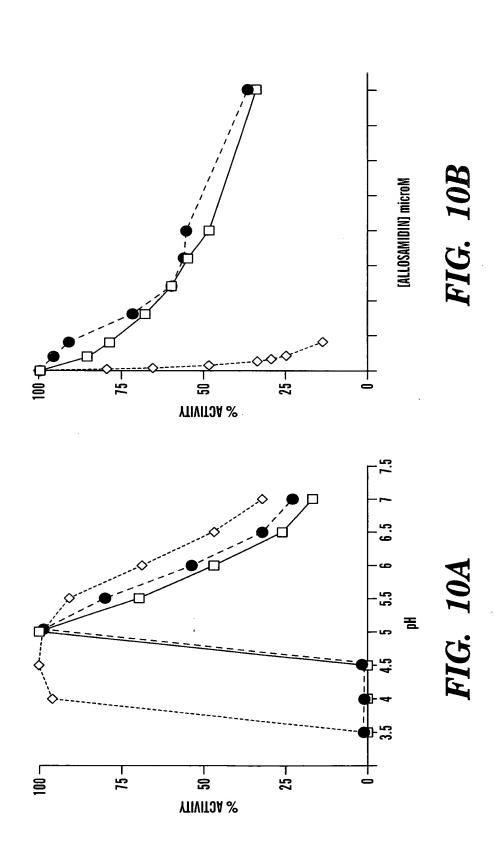




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FIG. 11

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DYYKHAIWKTRSYSIHAPGVDRYBWDLVKVCYBKICDGKAAHYYNTDYKBSSIIIWKGBPYLIKWWQQGP 540YGSYCGDGCNSRITYONYONINTODRKSPRQILBEYYOORKQGIIAGYYGSWNSQGDRAKEMI 125 -- NPNLNVVHMSPAKADLSYDSIESIVGSPLLPKSLIGLEYIGLNEYPNDAMNLRKARPDIIMLLSLGGE 140 IQTYNL-ETTNPDIMVDMYLSHLYPGLKYNITIILGFSLEHNRGGPSPENKELLELVGKTIHDKNQMNR 400 DSNPMVSILYIAPARINMLYDVSRPPNGRQRFILLRKHGLEYBTYGAMLNBIRRIRKVRPDVIILLSLGGB 195 TYHPSSPDSALNAVEKIANLVDELGPDGIDVDYEPNGSPDGLNDKEKADPFVQYVTKLREYMCDDKLISI 210 SQSSNGALSCI-GPNDPKKICHODBAPYNSKYPNKP-DVKKBLLRAAQMASAGGAIYLANNLLICHIDMVF 278 SGSSNAALSCVSGVAS---PCKDBBSPYNTKPLSBQIBTNKBLARAAAMLSAGTPINIPNTAKBKIDLVP 331 VQTPNYTNSTDSTVMCELYDSYAYYGKKYDYVIIMGPTLMPPSTPPNPNDKMLVKSIGDPVKTENKLNKR 348 ADGIGIWHLPMKEQLPTGSPDVDIPLTNIWHLNPEVQTPKDLTITENPEDCSTIDEYVPGLVIPTIGIN 470 TYM-IDIEKEIDYVDKILKLVNDPDLDGVDIDWEPHGKPYNLNELNPSNYYIKLINLLRKTIPEEKLISI 264 Pro-caly me domain MVXIIIVSILYSANSRT-----LKGKNNINNSLGIIRENKNKTHOTBIHESPSHLKSNNSNFVE 64 Substrate-binding site Chitin-binding domain Catalytic domain begins begins PEGGALESYTKLDASKCPGIBENNKKYPHKPLEVEEGYEGEVDLPLQ. 587 •••• ADGPCLWSLSSDNAAINRQLAIBYPVBSLH. 378 Active site Catalytic domain ends :: • PSCHT1 PSCHT1 PSCHT1 PSCH11 PSCH1 PECHI PSCH11 PgCHT1 Pfani PSCHIL PECHI POCH PCCHI PECHI PECATI

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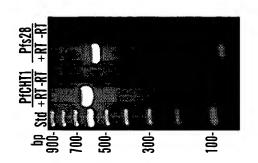


FIG. 12B

FIG. 12C



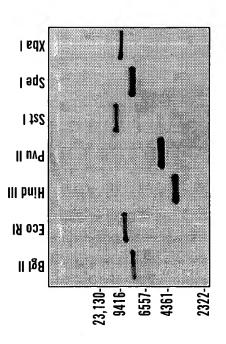


FIG. 12A



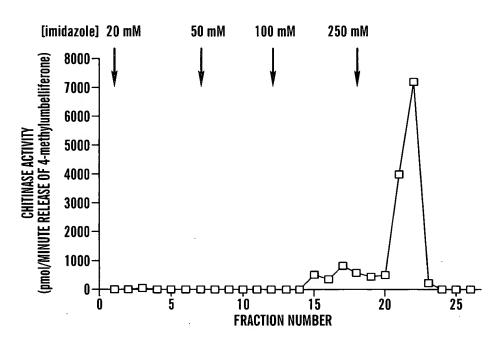
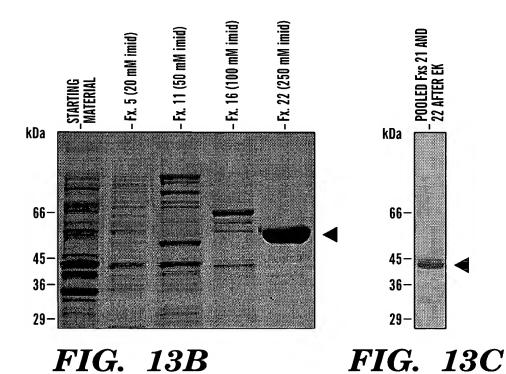


FIG. 13A





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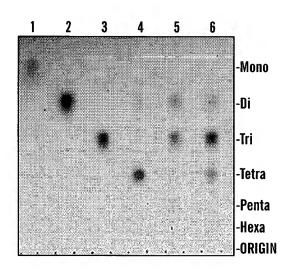


FIG. 14A

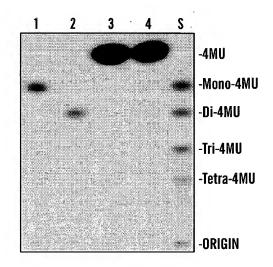


FIG. 14B

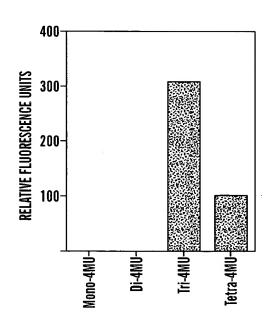


FIG. 14C



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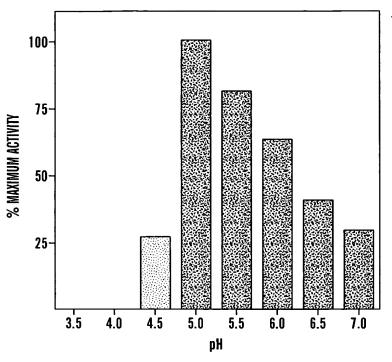


FIG. 15A

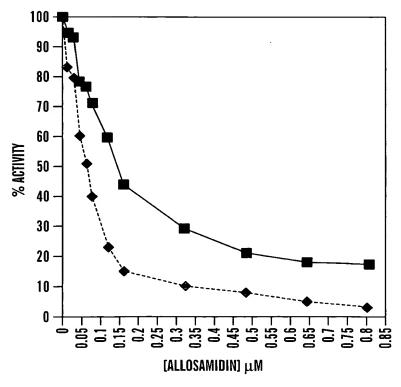


FIG. 15B



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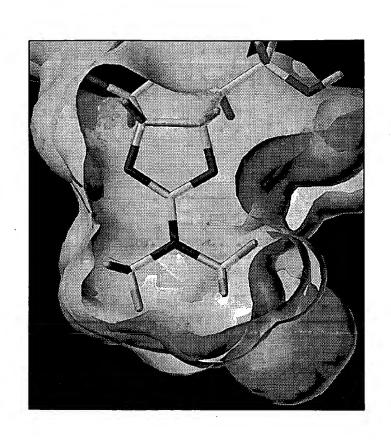


FIG. 16